

OIEP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/805,311

DATE: 03/30/2001

TIME: 15:06:22

Input Set : A:\0961D Sequence Listing.txt

Output Set: N:\CRF3\03302001\I805311.raw

ENTERED

4 <110> APPLICANT: Mahajan, Pramod B.
 7 <120> TITLE OF INVENTION: Rad2/FEN-1 Orthologues and Uses
 8 Thereof
 10 <130> FILE REFERENCE: 0961D
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/805,311
 C--> 12 <141> CURRENT FILING DATE: 2001-03-13
 12 <150> PRIOR APPLICATION NUMBER: 09/426,557
 13 <151> PRIOR FILING DATE: 1999-10-22
 15 <150> PRIOR APPLICATION NUMBER: 60/112,332
 16 <151> PRIOR FILING DATE: 1998-12-15
 18 <160> NUMBER OF SEQ ID NOS: 10
 20 <170> SOFTWARE: FastSEQ for Windows Version 3.0
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 1463
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Zea mays
 27 <220> FEATURE:
 28 <221> NAME/KEY: CDS
 29 <222> LOCATION: (85)...(1221)
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 33 cccgccacag ccgcccgcga cgag atg ggc atc aag ggt ttg acg aaa ctg 111
 34 Met Gly Ile Lys Gly Leu Thr Lys Leu
 35 1 5
 37 ctg gcg gac aat gcg ccc aag gcg atg aag gag cag aag ttc gag agc 159
 38 Leu Ala Asp Asn Ala Pro Lys Ala Met Lys Glu Gln Lys Phe Glu Ser
 39 10 15 20 25
 41 tac ttc ggc cgc aaa atc gcc gtc gac gcc agc atg agc ata tac cag 207
 42 Tyr Phe Gly Arg Lys Ile Ala Val Asp Ala Ser Met Ser Ile Tyr Gln
 43 30 35 40
 45 ttc ctg att gta gtt gga agg aca ggc atg gaa act ctc aca aat gaa 255
 46 Phe Leu Ile Val Val Gly Arg Thr Gly Met Glu Thr Leu Thr Asn Glu
 47 45 50 55
 49 gct ggt gaa gtc act agt cat ttg caa gga atg ttc aac cgg aca ata 303
 50 Ala Gly Glu Val Thr Ser His Leu Gln Gly Met Phe Asn Arg Thr Ile
 51 60 65 70
 53 aga tta ctg gaa gcg gga atc aag cca gtt tat gtt ttt gat ggc aag 351
 54 Arg Leu Leu Glu Ala Gly Ile Lys Pro Val Tyr Val Phe Asp Gly Lys
 55 75 80 85
 57 cct cct gat atg aag aaa caa gag ctt gct aaa aga tac tca aaa aga 399
 58 Pro Pro Asp Met Lys Lys Gln Glu Leu Ala Lys Arg Tyr Ser Lys Arg
 59 90 95 100 105
 61 gat gat gca acc aaa gat ctg act gag gca gta gag gta gga gat aaa 447
 62 Asp Asp Ala Thr Lys Asp Leu Thr Glu Ala Val Glu Val Gly Asp Lys
 63 110 115 120
 66 gat gcg att gaa aaa ttg agc aag agg act gta aag gtc aca agg caa 495
 67 Asp Ala Ile Glu Lys Leu Ser Lys Arg Thr Val Lys Val Thr Arg Gln

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68		125		130		135		
70	cac aac gaa gat tgt aaa cgg cta tta aga ctt atg ggg gtt cct gtt							543
71	His Asn Glu Asp Cys Lys Arg Leu Leu Arg Leu Met Gly Val Pro Val							
72		140		145		150		
74	gta gag gca cct tct gaa gca gaa gca gaa tgt gca gcc ctt tgc ata							591
75	Val Glu Ala Pro Ser Glu Ala Glu Ala Glu Cys Ala Ala Leu Cys Ile							
76		155		160		165		
78	aac gat aag gtg ttc gct gtt gct tca gaa gat atg gac tcc ctt act							639
79	Asn Asp Lys Val Phe Ala Val Ala Ser Glu Asp Met Asp Ser Leu Thr							
80		170		175		180		185
82	ttt ggg gct cca cgg ttc ctt cgt cat tta atg gat cca agt tcc aag							687
83	Phe Gly Ala Pro Arg Phe Leu Arg His Leu Met Asp Pro Ser Ser Lys							
84			190		195		200	
86	aaa ata cct gtg atg gaa ttt gat gtt gcc aag gtt ttg gag gag ctt							735
87	Lys Ile Pro Val Met Glu Phe Asp Val Ala Lys Val Leu Glu Glu Leu							
88		205		210		215		
90	gaa ctc acc atg gac cag ttc att gat ttg tgc atc ctg tgt gga tgt							783
91	Glu Leu Thr Met Asp Gln Phe Ile Asp Leu Cys Ile Leu Cys Gly Cys							
92		220		225		230		
94	gac tat tgt gat agc atc aaa ggt atc ggg ggg caa aca gct ctg aaa							831
95	Asp Tyr Cys Asp Ser Ile Lys Gly Ile Gly Gly Gln Thr Ala Leu Lys							
96		235		240		245		
98	ctt att cgt caa cat ggg tcc ata gaa agc atc ttg gag aat ctt aat							879
99	Leu Ile Arg Gln His Gly Ser Ile Glu Ser Ile Leu Glu Asn Leu Asn							
100		250		255		260		265
102	aaa gac aga tat caa att cct gag gac tgg cct tac caa gaa gct cga							927
103	Lys Asp Arg Tyr Gln Ile Pro Glu Asp Trp Pro Tyr Gln Glu Ala Arg							
104			270		275		280	
106	cgc ttg ttc aag gag cct aat gtc aca ttg gat att cct gag cta aaa							975
107	Arg Leu Phe Lys Glu Pro Asn Val Thr Leu Asp Ile Pro Glu Leu Lys							
108		285		290		295		
110	tgg act gca cct gat gag gag ggt ctc ata agt ttc ctg gta aaa gat							1023
111	Trp Thr Ala Pro Asp Glu Glu Gly Leu Ile Ser Phe Leu Val Lys Asp							
112		300		305		310		
114	aat ggt ttc aac gaa gat cgg gtg aca aag gcc ata gag aag atc aaa							1071
115	Asn Gly Phe Asn Glu Asp Arg Val Thr Lys Ala Ile Glu Lys Ile Lys							
116		315		320		325		
118	tct gcc aag aat aaa tog tgc caa gga aga ctc gag tcc ttt ttc aag							1119
119	Ser Ala Lys Asn Lys Ser Ser Gln Gly Arg Leu Glu Ser Phe Phe Lys							
120		330		335		340		345
122	cca act gcc acc aca tca gca ccg cta aaa cgg aag gag act tgc gat							1167
123	Pro Thr Ala Thr Thr Ser Ala Pro Leu Lys Arg Lys Glu Thr Ser Asp							
124		350		355		360		
128	aaa aca agc aag gca gct gcg aac aag aaa aca aag gct ggt gga aag							1215
129	Lys Thr Ser Lys Ala Ala Ala Asn Lys Lys Thr Lys Ala Gly Gly Lys							
130		365		370		375		
132	aag aaa taatcttggg tgcttgatgt acaactacga ctacgaaagc agcgggtggcg							1271
133	Lys Lys							
136	tgataccttc gcttagatta tttaactccc tgttttaact cagagctttg gtaaaagt							1331

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137 gctcatgtttt caagctgtggg taagtttagtt gtgtttgaag agattgggtgt accaagtaac 1391
138 aaaacttatc gctgtttttt acttcttgtc ctttgaagta aaaaaaaaaa aaaaaaaaaa 1451
139 aaaaaaaaaa aa 1463
141 <210> SEQ ID NO: 2
142 <211> LENGTH: 379
143 <212> TYPE: PRT
144 <213> ORGANISM: Zea mays
146 <400> SEQUENCE: 2
147 Met Gly Ile Lys Gly Leu Thr Lys Leu Leu Ala Asp Asn Ala Pro Lys
148 1 5 10 15
149 Ala Met Lys Glu Gln Lys Phe Glu Ser Tyr Phe Gly Arg Lys Ile Ala
150 20 25 30
151 Val Asp Ala Ser Met Ser Ile Tyr Gln Phe Leu Ile Val Val Gly Arg
152 35 40 45
153 Thr Gly Met Glu Thr Leu Thr Asn Glu Ala Gly Glu Val Thr Ser His
154 50 55 60
155 Leu Gln Gly Met Phe Asn Arg Thr Ile Arg Leu Leu Glu Ala Gly Ile
156 65 70 75 80
157 Lys Pro Val Tyr Val Phe Asp Gly Lys Pro Pro Asp Met Lys Lys Gln
158 85 90 95
159 Glu Leu Ala Lys Arg Tyr Ser Lys Arg Asp Asp Ala Thr Lys Asp Leu
160 100 105 110
161 Thr Glu Ala Val Glu Val Gly Asp Lys Asp Ala Ile Glu Lys Leu Ser
162 115 120 125
163 Lys Arg Thr Val Lys Val Thr Arg Gln His Asn Glu Asp Cys Lys Arg
164 130 135 140
165 Leu Leu Arg Leu Met Gly Val Pro Val Val Glu Ala Pro Ser Glu Ala
166 145 150 155 160
167 Glu Ala Glu Cys Ala Ala Leu Cys Ile Asn Asp Lys Val Phe Ala Val
168 165 170 175
169 Ala Ser Glu Asp Met Asp Ser Leu Thr Phe Gly Ala Pro Arg Phe Leu
170 180 185 190
171 Arg His Leu Met Asp Pro Ser Ser Lys Lys Ile Pro Val Met Glu Phe
172 195 200 205
173 Asp Val Ala Lys Val Leu Glu Glu Leu Glu Leu Thr Met Asp Gln Phe
174 210 215 220
175 Ile Asp Leu Cys Ile Leu Cys Gly Cys Asp Tyr Cys Asp Ser Ile Lys
176 225 230 235 240
177 Gly Ile Gly Gly Gln Thr Ala Leu Lys Leu Ile Arg Gln His Gly Ser
178 245 250 255
179 Ile Glu Ser Ile Leu Glu Asn Leu Asn Lys Asp Arg Tyr Gln Ile Pro
180 260 265 270
181 Glu Asp Trp Pro Tyr Gln Glu Ala Arg Arg Leu Phe Lys Glu Pro Asn
182 275 280 285
183 Val Thr Leu Asp Ile Pro Glu Leu Lys Trp Thr Ala Pro Asp Glu Glu
184 290 295 300
185 Gly Leu Ile Ser Phe Leu Val Lys Asp Asn Gly Phe Asn Glu Asp Arg
186 305 310 315 320
187 Val Thr Lys Ala Ile Glu Lys Ile Lys Ser Ala Lys Asn Lys Ser Ser

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188          325          330          335
190  Gln Gly Arg Leu Glu Ser Phe Phe Lys Pro Thr Ala Thr Thr Ser Ala
191          340          345          350
192  Pro Leu Lys Arg Lys Glu Thr Ser Asp Lys Thr Ser Lys Ala Ala Ala
193          355          360          365
194  Asn Lys Lys Thr Lys Ala Gly Gly Lys Lys Lys
195          370          375
197 <210> SEQ ID NO: 3
198 <211> LENGTH: 1541
199 <212> TYPE: DNA
200 <213> ORGANISM: Zea mays
202 <220> FEATURE:
203 <221> NAME/KEY: CDS
204 <222> LOCATION: (79)...(1215)
206 <400> SEQUENCE: 3
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208  acagcgcgcg cagacgag atg ggc atc aag ggt ttg acg aaa ctg ctg gcg 111
209          Met Gly Ile Lys Gly Leu Thr Lys Leu Leu Ala
210          1          5          10
212  gac aat gcg ccc aag gcg atg aag gag cag aag ttc gag agc tac ttc 159
213  Asp Asn Ala Pro Lys Ala Met Lys Glu Gln Lys Phe Glu Ser Tyr Phe
214          15          20          25
216  ggc cgc aaa atc gcc gtc gac gcc agc atg agc ata tac cag ttc ctg 207
217  Gly Arg Lys Ile Ala Val Asp Ala Ser Met Ser Ile Tyr Gln Phe Leu
218          30          35          40
220  att gta gtt gga agg aca gcc atg gaa act ctc aca aat gaa gct ggt 255
221  Ile Val Val Gly Arg Thr Gly Met Glu Thr Leu Thr Asn Glu Ala Gly
222          45          50          55
224  gaa gtc act agt cat ttg caa gga atg ttc aac cgg aca ata aga tta 303
225  Glu Val Thr Ser His Leu Gln Gly Met Phe Asn Arg Thr Ile Arg Leu
226          60          65          70          75
228  ctg gaa gcg gga atc aag cca gtt tat gtt ttt gat gcc aag cct cct 351
229  Leu Glu Ala Gly Ile Lys Pro Val Tyr Val Phe Asp Gly Lys Pro Pro
230          80          85          90
232  gat atg aag aaa caa gag ctt gct aaa aga tac tca aaa aga gat gat 399
233  Asp Met Lys Lys Gln Glu Leu Ala Lys Arg Tyr Ser Lys Arg Asp Asp
234          95          100          105
236  gca acc aaa gat ctg act gag gca gta gag gta gga gat aaa gat gcg 447
237  Ala Thr Lys Asp Leu Thr Glu Ala Val Glu Val Gly Asp Lys Asp Ala
238          110          115          120
240  att gaa aaa ttg agc aag agg act gta aag gtc aca agg caa cac aac 495
241  Ile Glu Lys Leu Ser Lys Arg Thr Val Lys Val Thr Arg Gln His Asn
242          125          130          135
244  gaa gat tgt aaa cgg cta tta aga ctt atg ggg gtt cct gtt gta gag 543
245  Glu Asp Cys Lys Arg Leu Leu Arg Leu Met Gly Val Pro Val Val Glu
246          140          145          150          155
248  gca cct tct gaa gca gaa gca gaa tgt gca gcc ctt tgc ata aac gat 591
249  Ala Pro Ser Glu Ala Glu Ala Glu Cys Ala Ala Leu Cys Ile Asn Asp
250          160          165          170

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252 aag gtg ttc gct gtt gct tca gaa gat atg gac tcc ctt act ttt ggg      639
253 Lys Val Phe Ala Val Ala Ser Glu Asp Met Asp Ser Leu Thr Phe Gly
254      175      180      185
256 gct cca cgg ttc ctt cgt cat tta atg gat cca agt tcc aag aaa ata      687
257 Ala Pro Arg Phe Leu Arg His Leu Met Asp Pro Ser Ser Lys Lys Ile
258      190      195      200
260 cct gtg atg gaa ttt gat gtt gcc aag gtt ttg gag gag ctt gaa ctc      735
261 Pro Val Met Glu Phe Asp Val Ala Lys Val Leu Glu Glu Leu Glu Leu
262      205      210      215
264 acc atg gac cag ttc att gat ttg tgc atc ctg tgt gga tgt gac tat      783
265 Thr Met Asp Gln Phe Ile Asp Leu Cys Ile Leu Cys Gly Cys Asp Tyr
266      220      225      230      235
268 tgt gat agc atc aaa ggt atc ggg ggg caa aca gct ctg aaa ctt att      831
269 Cys Asp Ser Ile Lys Gly Ile Gly Gly Gln Thr Ala Leu Lys Leu Ile
270      240      245      250
272 cgt caa cat ggg tcc ata gaa agc atc ttg gag aat ctt aat aaa gac      879
273 Arg Gln His Gly Ser Ile Glu Ser Ile Leu Glu Asn Leu Asn Lys Asp
274      255      260      265
276 aga tat caa att cct gag gac tgg cct tac caa gaa gct cga cgc ttg      927
277 Arg Tyr Gln Ile Pro Glu Asp Trp Pro Tyr Gln Glu Ala Arg Arg Leu
278      270      275      280
280 ttc aag gag cct aat gtc aca ttg gat att cct gag cta aaa tgg act      975
281 Phe Lys Glu Pro Asn Val Thr Leu Asp Ile Pro Glu Leu Lys Trp Thr
282      285      290      295
284 gca cct gat gag gag ggt ctc ata agt ttc ctg gta aaa gat aat ggt      1023
285 Ala Pro Asp Glu Glu Gly Leu Ile Ser Phe Leu Val Lys Asp Asn Gly
286      300      305      310      315
288 ttc aac gaa gat cgg gtg aga aag gcc ata gag aag atc aaa tct gcc      1071
289 Phe Asn Glu Asp Arg Val Arg Lys Ala Ile Glu Lys Ile Lys Ser Ala
290      320      325      330
292 aag aat aaa tcg tcg caa gga aga ctc gag tcc ttt ttc aag cca act      1119
293 Lys Asn Lys Ser Ser Gln Gly Arg Leu Glu Ser Phe Phe Lys Pro Thr
294      335      340      345
296 gcc acc aca tca gca ccg cta aaa cgg aag gag act tcg gat aaa aca      1167
297 Ala Thr Thr Ser Ala Pro Leu Lys Arg Lys Glu Thr Ser Asp Lys Thr
298      350      355      360
300 agc aag gca gct gcg aac aag aaa aca aag gct ggt gga aag aag aaa      1215
301 Ser Lys Ala Ala Ala Asn Lys Lys Thr Lys Ala Gly Gly Lys Lys Lys
302      365      370      375
304 taatcttgga tgcctgatgt acaactacga ctacgaaagc agcgggtggcg tgatcacttc      1275
305 gcttagatttta ttaactccc tgttttaact cagagctttg gtaaaagtgt gctcatgttt      1335
306 caagctgggg taagttagtt gtgtttgaag agattggtgt accaagtaac aaaacttatac      1395
307 gctgtttttt acttcctgtc ctttgaagta tgtatgccag tctctgtctt ttttaagtatc      1455
308 tgtgttgcaa caaaaattta aggccttgtt ttgatgcata ggctcacttt aagatttagt      1515
309 ttaaatattca aaaaaaaaaa aaaaaa      1541
314 <210> SEQ ID NO: 4
315 <211> LENGTH: 379
316 <212> TYPE: PRS
317 <213> ORGANISM: Zea mays

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VERIFICATION SUMMARY

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Input Set : A:\0961D Sequence Listing.txt

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date